

SEQUENCE LISTING

<110> University of Utah Research Foundation
Bock, Susan C.
Hobden, Adrian N.

<120> VARIANTS OF ANTITHROMBIN III

<130> 21101.0021P1

<150> 60/384,599

<151> 2002-05-31

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<210> 61

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<210> 67

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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
          20          25          30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
          35          40          45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
          50          55          60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65          70          75          80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
          85          90          95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
          100          105          110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
          115          120          125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
          130          135          140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145          150          155          160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
          165          170          175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
          180          185          190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
          195          200          205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
          210          215          220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225          230          235          240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
          245          250          255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
          260          265          270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
          275          280          285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
          290          295          300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305          310          315          320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
          325          330          335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
          340          345          350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
          355          360          365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
          370          375          380
Ala Leu Glu Ala Asn Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385          390          395          400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
          405          410          415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
          420          425          430

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<211> 29
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<400> 71
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<210> 73
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 Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
 35 40 45
 Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
 50 55 60
 Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
 65 70 75 80
 Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
 85 90 95
 Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
 100 105 110
 Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
 115 120 125
 Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130 135 140
 Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
 145 150 155 160
 Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
 165 170 175
 Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
 180 185 190
 Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
 195 200 205
 Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210 215 220
 Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
 225 230 235 240
 Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
 245 250 255
 Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
 260 265 270
 Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
 275 280 285
 Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290 295 300
 Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
 305 310 315 320

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Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
      325      330      335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
      340      345      350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
      355      360      365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
      370      375      380
Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385      390      395      400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
      405      410      415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
      420      425      430

```

<210> 78

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 78

```

Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1      5      10      15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
20      25      30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
35      40      45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
50      55      60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65      70      75      80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
85      90      95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
100      105      110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
115      120      125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
130      135      140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145      150      155      160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
165      170      175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
180      185      190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
195      200      205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210      215      220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225      230      235      240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
245      250      255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
260      265      270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
275      280      285

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Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290                295                300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                310                315                320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                330                335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
                340                345                350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
                355                360                365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
                370                375                380
Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                390                395                400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                410                415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
                420                425                430

```

<210> 79

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 79

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agccctgtgg acatctgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag      120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc      180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt      240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg      300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc      360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca      420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt      480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc      540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt      600
ccctcggaag ccataaatga gctcactgtt ctgggtgctg ttaacaccat ttacttcaag      660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct      720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc      780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc      840
ctcatcttgc ccaagcctga gaagagcctg gccaaagtgga agaaggaact caccacagag      900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tgggtggtcca catgccccgc      960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgctcgat      1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc      1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg      1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc      1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc      1260
atgggcagag tagccaaccc ttgtgttaag taa                                1293

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<210> 80

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<400> 80
 agtcccgtag atatatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt 60
 taccgctccc cggagaagaa ggcaactgag gatgagggtc cagaacagaa gatcccggag 120
 gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc 180
 tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240
 atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg 300
 atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc 360
 tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca 420
 gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480
 gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc 540
 agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt 600
 ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag 660
 ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct 720
 gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc 780
 gtggctgaag gcacccagggt gcttgagttg cccttcaaag gtgatgacat caccatggtc 840
 ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact caccacagag 900
 gtgctgcagg agtggtctga tgaattggag gagatgatgc tgggtgtcca catgccccgc 960
 ttccgcattg aggaacggctt cagtttgaag gagcagctgc aagacatggg ccttgctgat 1020
 ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc 1080
 tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg 1140
 gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc 1200
 aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc 1260
 atgggcagag tagccaaccc ttgtgttaag taa 1293

<210> 81

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 81

Ser	Pro	Val	Asp	Val	Cys	Thr	Ala	Lys	Pro	Arg	Asp	Ile	Pro	Met	Asn
1				5					10					15	
Pro	Met	Cys	Ile	Tyr	Arg	Ser	Pro	Glu	Lys	Lys	Ala	Thr	Glu	Asp	Glu
			20					25					30		
Gly	Ser	Glu	Gln	Lys	Ile	Pro	Glu	Ala	Thr	Asn	Arg	Arg	Val	Trp	Glu
		35				40					45				
Leu	Ser	Lys	Ala	Asn	Ser	Arg	Phe	Ala	Thr	Thr	Phe	Tyr	Gln	His	Leu
	50				55						60				
Ala	Asp	Ser	Lys	Asn	Asp	Asn	Asp	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser
65				70					75					80	
Ile	Ser	Thr	Ala	Phe	Ala	Met	Thr	Lys	Leu	Gly	Ala	Cys	Asn	Asp	Thr
			85					90					95		
Leu	Gln	Gln	Leu	Met	Glu	Val	Phe	Lys	Phe	Asp	Thr	Ile	Ser	Glu	Lys
		100						105					110		
Thr	Ser	Asp	Gln	Ile	His	Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu	
	115					120					125				
Tyr	Arg	Lys	Ala	Asn	Lys	Ala	Ser	Lys	Leu	Val	Ser	Ala	Asn	Arg	Leu
	130				135						140				
Phe	Gly	Asp	Lys	Ser	Leu	Thr	Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile	Ser
145				150					155					160	
Glu	Leu	Val	Tyr	Gly	Ala	Lys	Leu	Gln	Pro	Leu	Asp	Phe	Lys	Glu	Asn
			165					170					175		
Ala	Glu	Gln	Ser	Arg	Ala	Ala	Ile	Asn	Lys	Trp	Val	Ser	Asn	Lys	Thr
		180					185						190		
Glu	Gly	Arg	Ile	Thr	Asp	Val	Ile	Pro	Ser	Glu	Ala	Ile	Asn	Glu	Leu
	195					200						205			

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Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210                215                220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                230                235                240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                250                255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
                260                265                270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
                275                280                285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
                290                295                300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                310                315                320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                330                335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
                340                345                350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
                355                360                365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
                370                375                380
Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                390                395                400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                410                415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
                420                425                430

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<210> 82

<211> 1293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 82

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agccctgtgg acgtatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt      60
taccgctccc cggagaagaa ggcaactgag gatgagggtc cagaacagaa gatcccggag      120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc      180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt      240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg      300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc      360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca      420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt      480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc      540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt      600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag      660
ggcctgtgga agtcaaaagt cagccctgag aacacaagga aggaactgtt ctacaaggct      720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc      780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc      840
ctcatcttgc ccaagcctga gaagagcctg gccaaaggtg agaaggaact caccacagag      900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc      960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat      1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc      1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg      1140
gccgaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc      1200
aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc      1260
atgggcagag tagccaaccc ttgtgttaag taa                                1293

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<210> 83
 <211> 1293
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 83
 agtcccgtag atgtgtgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt 60
 taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag 120
 gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc 180
 tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt 240
 atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg 300
 atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc 360
 tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca 420
 gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt 480
 gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc 540
 agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt 600
 ccctcgggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag 660
 ggcctgtgga agtcaaagt cagccctgag aacacaagga aggaactgtt ctacaaggct 720
 gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc 780
 gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc 840
 ctcactttgc ccaagcctga gaagagcctg gccaaaggtg agaaggaact caccacagag 900
 gtgctgcagg agtggtctga tgaattggag gagatgatgc tgggtgtcca catgccccgc 960
 ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat 1020
 ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc 1080
 tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg 1140
 gccgcaagta ccgctctaga ggctcagggc cgctcgctaa accccaacag ggtgactttc 1200
 aaggccaaca ggcctttcct ggtttttata agagaagttc ctctgaacac tattatcttc 1260
 atgggcagag tagccaaccc ttgtgttaag taa 1293

<210> 84
 <211> 430
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 84
 Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1 5 10 15
 Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
 20 25 30
 Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
 35 40 45
 Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
 50 55 60
 Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
 65 70 75 80
 Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
 85 90 95
 Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
 100 105 110
 Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
 115 120 125

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Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130                      135                      140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                      150                      155                      160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                      165                      170                      175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
                      180                      185                      190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
                      195                      200                      205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
                      210                      215                      220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                      230                      235                      240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                      245                      250                      255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
                      260                      265                      270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
                      275                      280                      285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
290                      295                      300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                      310                      315                      320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                      325                      330                      335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
                      340                      345                      350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
                      355                      360                      365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
                      370                      375                      380
Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                      390                      395                      400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                      405                      410                      415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
                      420                      425                      430

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<210> 85

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 85

```

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1                      5                      10                      15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
                      20                      25                      30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
                      35                      40                      45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
50                      55                      60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65                      70                      75                      80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                      85                      90                      95

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Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
      100      105      110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
      115      120      125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
      130      135      140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145      150      155      160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
      165      170      175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
      180      185      190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
      195      200      205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
210      215      220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225      230      235      240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
      245      250      255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
      260      265      270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
      275      280      285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
290      295      300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305      310      315      320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
      325      330      335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
      340      345      350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
      355      360      365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
      370      375      380
Ser Thr Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val
385      390      395      400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
      405      410      415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
      420      425      430

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<210> 86

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 86

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His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1      5      10      15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
      20      25      30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
      35      40      45

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Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
  50          55          60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
  65          70          75          80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
          85          90          95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
          100          105          110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
          115          120          125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
          130          135          140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
          145          150          155          160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
          165          170          175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
          180          185          190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
          195          200          205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
          210          215          220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
          225          230          235          240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
          245          250          255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
          260          265          270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
          275          280          285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
          290          295          300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
          305          310          315          320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
          325          330          335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
          340          345          350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
          355          360          365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
          370          375          380
Ser Thr Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val
          385          390          395          400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
          405          410          415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
          420          425          430

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<210> 87

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 87

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His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
  1          5          10          15

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Met	Asn	Pro	Met 20	Cys	Ile	Tyr	Arg	Ser 25	Pro	Glu	Lys	Lys	Ala 30	Thr	Glu
Asp	Glu	Gly 35	Ser	Glu	Gln	Lys	Ile	Pro 40	Glu	Ala	Thr	Asn 45	Arg	Arg	Val
Trp	Glu	Leu	Ser	Lys	Ala	Asn 55	Ser	Arg	Phe	Ala	Thr 60	Thr	Phe	Tyr	Gln
His 65	Leu	Ala	Asp	Ser	Lys 70	Asn	Asp	Asn	Asp	Asn 75	Ile	Phe	Leu	Ser	Pro 80
Leu	Ser	Ile	Ser	Thr 85	Ala	Phe	Ala	Met	Thr 90	Lys	Leu	Gly	Ala	Cys 95	Asn
Asp	Thr	Leu	Gln 100	Gln	Leu	Met	Glu	Val 105	Phe	Lys	Phe	Asp	Thr 110	Ile	Ser
Glu	Lys	Thr 115	Ser	Asp	Gln	Ile	His 120	Phe	Phe	Phe	Ala	Lys 125	Leu	Asn	Cys
Arg	Leu 130	Tyr	Arg	Lys	Ala	Asn 135	Lys	Ser	Ser	Lys	Leu 140	Val	Ser	Ala	Asn
Arg 145	Leu	Phe	Gly	Asp	Lys 150	Ser	Leu	Thr	Phe	Asn 155	Glu	Thr	Tyr	Gln	Asp 160
Ile	Ser	Glu	Leu 165	Val	Tyr	Gly	Ala	Lys 170	Leu	Gln	Pro	Leu	Asp 175	Phe	Lys
Glu	Asn	Ala 180	Glu	Gln	Ser	Arg	Ala 185	Ala	Ile	Asn	Lys	Trp 190	Val	Ser	Asn
Lys	Thr 195	Glu	Gly	Arg	Ile	Thr	Asp 200	Val	Ile	Pro	Ser	Glu 205	Ala	Ile	Asn
Glu	Leu 210	Thr	Val	Leu	Val	Leu 215	Val	Asn	Thr	Ile	Tyr 220	Phe	Lys	Gly	Leu
Trp 225	Lys	Ser	Lys	Phe	Ser 230	Pro	Glu	Asn	Thr	Arg 235	Lys	Glu	Leu	Phe	Tyr 240
Lys	Ala	Asp	Gly 245	Glu	Ser	Cys	Ser	Ala 250	Ser	Met	Met	Tyr	Gln 255	Glu	Gly
Lys	Phe	Arg	Tyr 260	Arg	Arg	Val	Ala 265	Glu	Gly	Thr	Gln	Val 270	Leu	Glu	Leu
Pro	Phe	Lys 275	Gly	Asp	Asp	Ile	Thr 280	Met	Val	Leu	Ile	Leu 285	Pro	Lys	Pro
Glu	Lys 290	Ser	Leu	Ala	Lys	Val 295	Glu	Lys	Glu	Leu	Thr 300	Pro	Glu	Val	Leu
Gln 305	Glu	Trp	Leu	Asp	Glu 310	Leu	Glu	Glu	Met	Met 315	Leu	Val	Val	His	Met 320
Pro	Arg	Phe	Arg 325	Ile	Glu	Asp	Gly	Phe 330	Ser	Leu	Lys	Glu	Gln 335	Leu	Gln
Asp	Met	Gly	Leu 340	Val	Asp	Leu	Phe	Ser 345	Pro	Glu	Lys	Ser	Lys 350	Leu	Pro
Gly	Ile	Val 355	Ala	Glu	Gly	Arg	Asp 360	Asp	Leu	Tyr	Val	Ser 365	Asp	Ala	Phe
His	Lys 370	Ala	Phe	Leu	Glu	Val 375	Asn	Glu	Glu	Gly	Ser 380	Glu	Ala	Ala	Ala
Ser 385	Thr	Ala	Leu	Glu	Ala 390	Tyr	Gly	Arg	Ser	Leu 395	Asn	Pro	Asn	Arg	Val 400
Thr	Phe	Lys	Ala 405	Asn	Arg	Pro	Phe	Leu 410	Val	Phe	Ile	Arg	Glu 415	Val	Pro
Leu	Asn	Thr	Ile 420	Phe	Met	Gly	Arg 425	Val	Ala	Asn	Pro	Cys 430	Val	Lys	

<210> 88

<211> 423

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence:/note =

ATTORNEY DOCKET NO. 21101.0021P1

synthetic construct

<400> 88

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Arg Asp Ile Pro Val Asn Pro Ile Cys Ile Tyr Arg Asn Pro Glu Lys
 1           5           10           15
Lys Pro Gln Glu Arg Arg Gly Ala Gly Ala Gly Glu Gly Gln Asp Pro
 20           25           30
Gly Val His Lys Pro Pro Val Trp Glu Leu Ser Arg Ala Asn Ser Arg
 35           40           45
Phe Ala Val Val Phe Tyr Lys His Leu Ala Asp Ser Lys Asp Asn Glu
 50           55           60
Glu Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser Thr Ala Phe Ala Met
 65           70           75           80
Thr Lys Leu Gly Ala Cys Gly Asp Thr Leu Gln Gln Leu Met Glu Val
 85           90           95
Phe Gln Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Val His Phe
100           105           110
Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Lys Lys Ala Asn Lys Ser
115           120           125
Ser Glu Leu Ile Ser Ala Asn Arg Leu Phe Gly Glu Lys Ser Leu Val
130           135           140
Phe Asn Glu Thr Tyr Gln Asn Ile Ser Glu Ile Val Tyr Gly Ala Lys
145           150           155           160
Leu Trp Pro Leu Asn Phe Lys Glu Lys Pro Glu Leu Ser Arg Lys Ile
165           170           175
Ile Asn Glu Trp Val Ala Asn Lys Thr Glu Arg Arg Ile Thr Glu Val
180           185           190
Ile Pro Glu Lys Gly Ile Asp Asp Leu Thr Val Leu Val Leu Val Asn
195           200           205
Thr Ile Tyr Phe Lys Gly His Trp Lys Ser Gln Phe Pro Ala Pro Asn
210           215           220
Thr Arg Leu Asp Leu Phe His Lys Ala Asn Gly Glu Thr Cys Asn Val
225           230           235           240
Pro Ile Met Tyr Gln Glu Ser Arg Phe Pro Tyr Ala Phe Ile Gln Glu
245           250           255
Asp Lys Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
260           265           270
Met Val Leu Val Leu Pro Lys Ala Gly Thr Pro Leu Val Glu Val Glu
275           280           285
Arg Asp Leu Thr Ser Asp Lys Leu Gln Asp Trp Ile Asp Ser Met Met
290           295           300
Glu Val Ser Leu Thr Val Ser Phe Pro Arg Phe Arg Val Glu Asp Ser
305           310           315           320
Phe Ser Val Lys Glu Lys Leu Arg Lys Met Gly Leu Glu Asp Leu Phe
325           330           335
Ser Pro Glu Asn Ala Lys Leu Pro Gly Ile Val Ala Gly Asp Arg Thr
340           345           350
Asp Leu Tyr Val Ser Glu Ala Phe His Lys Ala Phe Leu Glu Val Asn
355           360           365
Glu Glu Gly Ser Glu Ala Ser Ala Ala Thr Ala Val Val Ile Ser Gly
370           375           380
Arg Ser Phe Pro Met Asn Arg Ile Ile Phe Glu Ala Asn Arg Pro Phe
385           390           395           400
Leu Leu Phe Ile Arg Glu Ala Thr Leu Asn Thr Ile Ile Phe Met Gly
405           410           415
Arg Ile Ser Asp Pro Cys Ser
420

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<210> 89

<211> 456

ATTORNEY DOCKET NO. 21101.0021P1

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 89

Met	Tyr	Leu	Leu	Ser	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Gly	Ser	Ala	Tyr	1	5	10	15
Leu	Gln	Pro	Gln	His	Ala	Asp	Ile	Cys	Leu	Ala	Lys	Pro	Lys	Asp	Ile	20	25	30	
Pro	Leu	Thr	Pro	Met	Cys	Val	Tyr	Arg	Lys	Pro	Leu	Glu	Val	Val	Glu	35	40	45	
Thr	Glu	Glu	Lys	Glu	Lys	Glu	Pro	Thr	Thr	Gln	Glu	Gln	Lys	Val	Pro	50	55	60	
Glu	Ser	Thr	Asn	Pro	Arg	Val	Tyr	Glu	Leu	Ser	Gln	Ala	Asn	Ala	Lys	65	70	75	80
Phe	Ala	Ile	Ala	Phe	Tyr	Lys	Asn	Leu	Ala	Asp	Ser	Lys	Arg	Asp	Lys	85	90	95	
Glu	Asn	Ile	Phe	Met	Ser	Pro	Leu	Ser	Ile	Ser	Gln	Ala	Phe	Thr	Met	100	105	110	
Ala	Lys	Leu	Gly	Ala	Cys	Asn	Asn	Thr	Leu	Lys	Gln	Leu	Met	Glu	Val	115	120	125	
Phe	His	Phe	Asp	Thr	Val	Ser	Glu	Arg	Ala	Ser	Asp	Gln	Ile	His	Tyr	130	135	140	
Phe	Phe	Ala	Lys	Leu	Asn	Cys	Arg	Leu	Phe	Arg	Lys	Ala	Asn	Lys	Ser	145	150	155	160
Ser	Glu	Leu	Val	Ser	Val	Asn	Arg	Leu	Phe	Gly	Glu	Lys	Ser	Leu	Thr	165	170	175	
Phe	Asn	Glu	Thr	Tyr	Gln	Asp	Ile	Ser	Glu	Ile	Val	Tyr	Gly	Ala	Lys	180	185	190	
Leu	Trp	Pro	Leu	Asn	Phe	Arg	Asp	Lys	Pro	Glu	Leu	Ser	Arg	Glu	Ile	195	200	205	
Ile	Asn	Asn	Trp	Val	Ser	Asn	Lys	Thr	Glu	Lys	Arg	Ile	Thr	Asp	Val	210	215	220	
Ile	Pro	Lys	Asp	Ala	Ile	Thr	Pro	Asp	Thr	Val	Leu	Val	Leu	Ile	Asn	225	230	235	240
Ala	Ile	Tyr	Phe	Lys	Gly	Leu	Trp	Lys	Ser	Lys	Phe	Asn	Ser	Glu	Asn	245	250	255	
Thr	Lys	Met	Asp	Gln	Phe	His	Pro	Ala	Lys	Asn	Ser	Asn	Cys	Leu	Thr	260	265	270	
Ala	Thr	Met	Tyr	Gln	Glu	Gly	Thr	Phe	Arg	Tyr	Gly	Ser	Phe	Lys	Asp	275	280	285	
Asp	Gly	Val	Gln	Val	Leu	Glu	Leu	Pro	Tyr	Lys	Gly	Asp	Asp	Ile	Thr	290	295	300	
Met	Val	Leu	Val	Leu	Pro	Ser	Gln	Glu	Thr	Pro	Leu	Thr	Thr	Val	Glu	305	310	315	320
Gln	Asn	Leu	Thr	Leu	Glu	Lys	Leu	Gly	Asn	Trp	Leu	Gln	Lys	Ser	Arg	325	330	335	
Glu	Leu	Gln	Leu	Ser	Val	Tyr	Leu	Pro	Arg	Phe	Arg	Val	Glu	Asp	Ser	340	345	350	
Phe	Ser	Val	Lys	Glu	Lys	Leu	Gln	Glu	Met	Gly	Leu	Val	Asp	Leu	Phe	355	360	365	
Asp	Pro	Asn	Ser	Ala	Lys	Leu	Pro	Gly	Ile	Ile	Ala	Gly	Gly	Arg	Thr	370	375	380	
Asp	Leu	Tyr	Val	Ser	Asp	Ala	Phe	His	Lys	Ala	Phe	Leu	Glu	Val	Asn	385	390	395	400
Glu	Glu	Gly	Ser	Glu	Ala	Ala	Ala	Ser	Thr	Ala	Val	Ile	Leu	Thr	Gly	405	410	415	

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Arg Ser Leu Asn Leu Asn Arg Ile Ile Phe Arg Ala Asn Arg Pro Phe
 420 425 430
 Leu Val Phe Ile Arg Glu Val Ala Ile Asn Ala Ile Leu Phe Met Gly
 435 440 445
 Arg Val Ala Asn Pro Cys Thr Glu
 450 455

<210> 90

<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 90

Met Tyr Ser Pro Gly Ala Gly Ser Gly Ala Ala Gly Glu Arg Lys Leu
 1 5 10 15
 Cys Leu Leu Ser Leu Leu Leu Ile Gly Ala Leu Gly Cys Ala Ile Cys
 20 25 30
 His Gly Asn Pro Val Asp Asp Ile Cys Ile Ala Lys Pro Arg Asp Ile
 35 40 45
 Pro Val Asn Pro Leu Cys Ile Tyr Arg Ser Pro Gly Lys Lys Ala Thr
 50 55 60
 Glu Glu Asp Gly Ser Glu Gln Lys Val Pro Glu Ala Thr Asn Arg Arg
 65 70 75 80
 Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Asn Phe Tyr
 85 90 95
 Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser
 100 105 110
 Pro Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys
 115 120 125
 Asn Asp Thr Leu Lys Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile
 130 135 140
 Ser Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn
 145 150 155 160
 Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Asp Leu Val Ser Ala
 165 170 175
 Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Ser Tyr Gln
 180 185 190
 Asp Val Ser Glu Val Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
 195 200 205
 Lys Glu Asn Pro Glu Gln Ser Arg Val Thr Ile Asn Asn Trp Val Ala
 210 215 220
 Asn Lys Thr Glu Gly Arg Ile Lys Asp Val Ile Pro Gln Gly Ala Ile
 225 230 235 240
 Asn Glu Leu Thr Ala Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly
 245 250 255
 Leu Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Pro Phe
 260 265 270
 Tyr Lys Val Asp Gly Gln Ser Cys Pro Val Pro Met Met Tyr Gln Glu
 275 280 285
 Gly Lys Phe Lys Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu
 290 295 300
 Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
 305 310 315 320
 Pro Glu Lys Ser Leu Ala Lys Val Glu Gln Glu Leu Thr Pro Glu Leu
 325 330 335
 Leu Gln Glu Trp Leu Asp Glu Leu Ser Glu Thr Met Leu Val Val His
 340 345 350

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Met Pro Arg Phe Arg Thr Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu
 355 360 365
 Gln Asp Met Gly Leu Ile Asp Leu Phe Ser Pro Glu Lys Ser Gln Leu
 370 375 380
 Pro Gly Ile Val Ala Gly Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala
 385 390 395 400
 Phe His Lys Ala Phe Leu Glu Val Asn Glu Gly Ser Glu Ala Ala
 405 410 415
 Ala Ser Thr Ser Val Val Ile Thr Gly Arg Ser Leu Asn Pro Asn Arg
 420 425 430
 Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Leu Ile Arg Glu Val
 435 440 445
 Ala Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val
 450 455 460
 Asn
 465

<210> 91

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 91

caccagcattc	atctcctcca	attcatccag	ctactctgcc	catgaagata	atagttttca	60
ggcggattgc	ctcagatcac	actatctcca	cttgcccagc	cctgtggaag	attagcggcc	120
atgtattcca	atgtgatagg	aactgtaacc	tctggaaaaa	ggaagggtta	tcttttgtcc	180
ttgctgctca	ttggcttctg	ggactgctg	acctgtcacg	ggagccctgt	ggacatctgc	240
acagccaagc	cgcgggacat	tcccatgaat	cccatgtgca	tttaccgctc	cccgagaag	300
aaggcaactg	aggatgaggg	ctcagaacag	aagatcccgg	aggccacca	ccggcgtgct	360
tgggaactgt	ccaaggccaa	ttcccgttt	gctaccactt	tctatcagca	cctggcagat	420
tccaagaatg	acaatgataa	cattttcctg	tcacccctga	gtatctccac	ggcttttgtct	480
atgaccaagc	tgggtgcctg	taatgacacc	ctccagcaac	tgatggaggt	atttaagttt	540
gacaccatat	ctgagaaaac	atctgatcag	atccacttct	tctttgccaa	actgaactgc	600
cgactctatc	gaaaagccaa	caaatcctcc	aagttagtag	cagccaatcg	cctttttgga	660
gacaaatccc	ttaccttcaa	tgagacctac	caggacatca	gtgagttggg	atatggagcc	720
aagctccagc	ccctggactt	caaggaaaat	gcagagcaat	ccagagcggc	catcaacaaa	780
tgggtgtcca	ataagaccga	aggccgaatc	accgatgtca	ttccctcgga	agccatcaat	840
gagctcactg	ttctggtgct	ggttaacacc	atttacttca	agggcctgtg	gaagtcaaag	900
ttcagccctg	agaacacaag	gaaggaaactg	ttctacaagg	ctgatggaga	gtcgtgttca	960
gcatctatga	tgtaccagga	aggcaagttc	cgttatcggc	gcgtggctga	aggcaccag	1020
gtgcttgagt	tgcccttcaa	aggatgatgac	atcaccatgg	tcctcatctt	gccaagcct	1080
gagaagagcc	tggccaaggt	ggagaaggaa	ctcaccocag	agggtgctga	ggagtggctg	1140
gatgaattgg	aggagatgat	gctgggtggt	cacatgcccc	gcttccgcat	tgaggacggc	1200
ttcagtttga	aggagcagct	gcaagacatg	ggccttgctg	atctgttcag	ccctgaaaag	1260
tccaaactcc	caggtattgt	tgacagaaggc	cgagatgacc	tctatgtctc	agatgcattc	1320
cataaggcat	ttcttgaggt	aaatgaagaa	ggcagtgaag	cagctgcaag	taccgctgtt	1380
gtgattgctg	gccgttcgct	aaaccccaac	agggtgactt	tcaaggccaa	caggcccttc	1440
ctgggtttta	taagagaagt	tcctctgaac	actattatct	tcatgggcag	agtagccaac	1500
ccttggtgta	agtaaaatgt	tcttattctt	tgcacctctt	cctatttttg	gtttgtgaac	1560
agaagtaaaa	ataaatacaa	actacttcca	tctcacatt			1599

<210> 92

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

Ser 1	Pro	Val	Asp	Ile 5	Cys	Thr	Ala	Lys	Pro 10	Arg	Asp	Ile	Pro	Met 15	Asn
Pro	Met	Cys	Ile 20	Tyr	Arg	Ser	Pro	Glu 25	Lys	Lys	Ala	Thr 30	Glu	Asp	Glu
Gly	Ser	Glu 35	Gln	Lys	Ile	Pro	Glu 40	Ala	Thr	Asn	Arg	Arg 45	Val	Trp	Glu
Leu	Ser 50	Lys	Ala	Asn	Ser	Arg 55	Phe	Ala	Thr	Thr	Phe 60	Tyr	Gln	His	Leu
Ala 65	Asp	Ser	Lys	Asn	Asp 70	Asn	Asp	Asn	Ile	Phe 75	Leu	Ser	Pro	Leu	Ser 80
Ile	Ser	Thr	Ala 85	Phe	Ala	Met	Thr	Lys	Leu 90	Gly	Ala	Cys	Asn	Asp 95	Thr
Leu	Gln	Gln 100	Leu	Met	Glu	Val	Phe	Lys 105	Phe	Asp	Thr	Ile	Ser 110	Glu	Lys
Thr	Ser	Asp 115	Gln	Ile	His	Phe	Phe 120	Phe	Ala	Lys	Leu	Asn 125	Cys	Arg	Leu
Tyr	Arg 130	Lys	Ala	Asn	Lys	Ala 135	Ser	Lys	Leu	Val	Ser 140	Ala	Asn	Arg	Leu
Phe 145	Gly	Asp	Lys	Ser	Leu 150	Thr	Phe	Asn	Glu	Thr 155	Tyr	Gln	Asp	Ile	Ser 160
Glu	Leu	Val	Tyr 165	Gly	Ala	Lys	Leu	Gln	Pro 170	Leu	Asp	Phe	Lys	Glu 175	Asn
Ala	Glu	Gln 180	Ser	Arg	Ala	Ala	Ile	Asn 185	Lys	Trp	Val	Ser	Asn 190	Lys	Thr
Glu	Gly	Arg 195	Ile	Thr	Asp	Val	Ile 200	Pro	Ser	Glu	Ala	Ile 205	Asn	Glu	Leu
Thr 210	Val	Leu	Val	Leu	Val	Asn 215	Thr	Ile	Tyr	Phe	Lys 220	Gly	Leu	Trp	Lys
Ser 225	Lys	Phe	Ser	Pro	Glu 230	Asn	Thr	Arg	Lys	Glu	Leu	Phe	Tyr	Lys	Ala 240
Asp	Gly	Glu	Ser 245	Cys	Ser	Ala	Ser	Met	Met 250	Tyr	Gln	Glu	Gly	Lys	Phe 255
Arg	Tyr	Arg 260	Val	Ala	Glu	Gly	Thr 265	Gln	Val	Leu	Glu	Leu	Pro	Glu	Phe
Lys	Gly	Asp 275	Asp	Ile	Thr	Met	Val 280	Leu	Ile	Leu	Pro	Lys 285	Pro	Glu	Lys
Ser 290	Leu	Ala	Lys	Val	Glu	Lys 295	Glu	Leu	Thr	Pro	Glu	Val	Leu	Gln	Glu
Trp 305	Leu	Asp	Glu	Leu	Glu 310	Glu	Met	Met	Leu	Val	Val	His	Met	Pro	Arg 320
Phe	Arg	Ile	Glu 325	Asp	Gly	Phe	Ser	Leu	Lys 330	Glu	Gln	Leu	Gln	Asp	Met 335
Gly	Leu	Val 340	Asp	Leu	Phe	Ser	Pro	Glu 345	Lys	Ser	Lys	Leu	Pro	Gly	Ile
Val	Ala	Glu 355	Gly	Arg	Asp	Asp	Leu 360	Tyr	Val	Ser	Asp	Ala 365	Phe	His	Lys
Ala	Phe 370	Leu	Glu	Val	Asn	Glu 375	Glu	Gly	Ser	Glu	Ala 380	Ala	Ala	Ser	Thr
Ala 385	Xaa	Xaa	Xaa	Xaa 390	Gly	Arg	Ser	Leu	Asn	Pro 395	Asn	Arg	Val	Thr	Phe 400
Lys	Ala	Asn	Arg 405	Pro	Phe	Leu	Val	Phe	Ile 410	Arg	Glu	Val	Pro	Leu	Asn 415

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Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
 420 425 430

<210> 93

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 93

Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
 1 5 10 15
 Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
 20 25 30
 Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
 35 40 45
 Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
 50 55 60
 Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
 65 70 75 80
 Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
 85 90 95
 Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
 100 105 110
 Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
 115 120 125
 Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
 130 135 140
 Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
 145 150 155 160
 Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
 165 170 175
 Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
 180 185 190
 Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
 195 200 205
 Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
 210 215 220
 Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
 225 230 235 240
 Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
 245 250 255
 Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
 260 265 270
 Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
 275 280 285
 Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
 290 295 300
 Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg
 305 310 315 320
 Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
 325 330 335
 Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
 340 345 350
 Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
 355 360 365
 Ala Phe Leu Glu Val Asn Glu Gly Ser Glu Ala Ala Ala Ser Thr
 370 375 380

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Ala	Val	Val	Ile	Ala	Gly	Arg	Ser	Leu	Asn	Pro	Asn	Arg	Val	Thr	Phe
385					390					395					400
Lys	Ala	Asn	Arg	Pro	Phe	Leu	Val	Phe	Ile	Arg	Glu	Val	Pro	Leu	Asn
				405					410					415	
Thr	Ile	Ile	Phe	Met	Gly	Arg	Val	Ala	Asn	Pro	Cys	Val	Lys		
			420					425					430		